L Number	Hits	Search Text	DB	Time stamp
1	3	penner-reinhold.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:25
2	2	fleig-andrea.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:25
3	10	ltrpc2	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:26
4	1	wo adj "200029571"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:51
5	1	wo adj "200040614"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:27
6	2	6548272.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:51

10007706 Results:

SEQ ID NO: 1

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7950	100.0	1503	3	AAY92944	Aay92944 Human TRP
2	7950	100.0	1503	3	AAY95439	Aay95439 Human cal
3	7950	100.0	1503	3	AAB36865	Aab36865 Human put
4	7950	100.0	1503	5	ABB76459	Abb76459 Human lon
5	7950	100.0	1503	5	ABB84544	Abb84544 Human tra
6	7950	100.0	1503	7	ADC47022	Adc47022 Human LTR
7	7950	100.0	1503	7	ADC77685	Adc77685 Human 222
8	7950	100.0	1503	7	ADC83633	Adc83633 LTRPC3-re
9	7741	97.4	1469	6	ABR43185	Abr43185 Human REM
10	6740.5	84.8	1508	7	ADC47024	Adc47024 Rat LTRPC
11	6709	84.4	1507	7	ADC47034	Adc47034 Mouse LTR
12	2771	34.9	525	6	ADA56830	Ada56830 Human sec
13	2771	34.9	525	6	ABR47695	Abr47695 Human sec
14	2771	34.9	525	6	ABR00046	Abr00046 Human gen
15	2771	34.9	525	7	ADB91501	Adb91501 Human sec
16	2771	34.9	525	7	ADC74074	Adc74074 Human sec

RESULT 1
AAY92944
ID   AAY92944 standard; protein; 1503 AA.
XX
AC   AAY92944;
XX
DT   08-NOV-2000   (first entry)
XX
DE   Human TRPC7 protein.
XX
KW   Transmembrane protein; TRPC7; brain; transient receptor potential; TRP;
KW   calcium channel function; human; gene therapy; periodic psychosis;
KW   mutation.
XX
OS   Homo sapiens.
XX
PN   WO200029571-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-JP006289.
XX
PR   12-NOV-1998;   98JP-00321200.
XX
PA   (EIKE) EIKEN KAGAKU KK.
XX
PI   Shimizu N,   Nagamine K;
XX
DR   WPI; 2000-387784/33.
DR   N-PSDB; AAA11284.
XX
PT   Nucleic acids encoding transmembrane protein TRPC7 expressed in brain and
PT   homologous to transient receptor potential protein useful in the of
PT   treatment of associated diseases such as periodic psychosis.
XX
PS   Claim 1; Page 64-71; 77pp; Japanese.
XX
CC   The invention relates to the isolation of a nucleic acid encoding a
CC   transmembrane protein TRPC7 which is expressed in brain and is homologous
CC   to transient receptor potential (TRP) protein. This suggests that the
CC   TRPC7 protein may have a calcium channel function. This sequence
CC   represents the human TRPC7 protein. The DNA and protein can be used in
CC   the diagnosis and treatment of disorders associated with TRPC7,

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    Query Match              100.0%;   Score 7950;   DB 3;   Length 1503;
    Best Local Similarity    100.0%;   Pred. No. 0;
    Matches 1503;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60

Qy      61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120

Qy     121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180

Qy     181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240

Qy     241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300

Qy     301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA 360

Qy     361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420

Qy     421 EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK 480

Qy     481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540

Qy     541 VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ 600

Qy     601 GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660

Qy     661 ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720

Qy     721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780

Qy     781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840

Qy     841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900

Qy     901 LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE 960
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE  960

Qy      961  RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF  1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF  1020

Qy     1021  PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA  1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA  1080

Qy     1081  PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ  1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ  1140

Qy     1141  KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA  1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA  1200

Qy     1201  SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE  1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE  1260

Qy     1261  KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ  1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ  1320

Qy     1321  AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP  1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP  1380

Qy     1381  LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI  1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI  1440

Qy     1441  ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG  1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG  1500

Qy     1501  AHY  1503
             |||
Db     1501  AHY  1503
```

RESULT 2
AAY95439
ID   AAY95439 standard; protein; 1503 AA.
XX
AC   AAY95439;
XX
DT   10-OCT-2000   (first entry)
XX
DE   Human calcium channel polypeptide.
XX
KW   Human; SOC-2/CRAC-1; calcium channel; store operated channel;
KW   calcium release activated channel; therapy; diagnosis;
KW   lymphocyte proliferative disorder.
XX
OS   Homo sapiens.
XX
PN   WO200040614-A2.
XX
PD   13-JUL-2000.
XX
PF   20-DEC-1999;   99WO-US029996.
XX
PR   30-DEC-1998;   98US-0114220P.
PR   29-JAN-1999;   99US-0120018P.
PR   22-JUN-1999;   99US-0140415P.

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XX
PA    (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI    Scharenberg AM;
XX
DR    WPI; 2000-465957/40.
DR    N-PSDB; AAA49926.
XX
PT    New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT    diagnose and treat proliferative disorders associated with the channel,
PT    and to screen for novel modulators of the channel.
XX
PS    Example; Page 69-72; 108pp; English.
XX
CC    The present sequence is that of a human calcium channel polypeptide as
CC    deduced from a cDNA clone (see AAA49926) identified in an EST database
CC    search for sequences showing homology to Caenorhabditis elegans calcium
CC    signal sequences. Clones isolated from such screenings were used to
CC    identify human clones (see AAA49922-24) encoding members (see AAY95435-
CC    37) of a new family of SOC (store operated channel) or CRAC (calcium
CC    release activated channel) calcium channel polypeptides. SOC/CRAC
CC    polypeptides modulate Ca2+ flux into and out of a cell, and may be
CC    activated upon depletion of Ca2+ from intracellular calcium stores,
CC    allowing Ca2+ influx into a cell. SOC/CRAC polypeptides and
CC    polynucleotides can be used to treat patients that require modulation of
CC    calcium influx into their SOC/CRAC-expressing cells. Polypeptides can be
CC    used to deliver therapeutic and/or imaging agents to such cells to
CC    modulate proliferation and growth. SOC/CRAC polypeptides also represent
CC    targets for designing and/or identifying inhibitors that block lymphocyte
CC    proliferation and binding agents that selectively bind to SOC/CRAC
CC    polypeptides to which drugs or toxins can be conjugated for delivery to
CC    SOC/CRAC expressing cells
XX
SQ    Sequence 1503 AA;

   Query Match            100.0%;  Score 7950;  DB 3;  Length 1503;
   Best Local Similarity  100.0%;  Pred. No. 0;
   Matches 1503;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60


RESULT 3
AAB36865
ID    AAB36865 standard; protein; 1503 AA.
XX
AC    AAB36865;
XX
DT    21-FEB-2001   (first entry)
XX
DE    Human putative Ca2+ channel protein TrpC7 protein.
XX
KW    mutTCCH-1; sugar-phosphate hydrolase; NUDT9.
XX
OS    Homo sapiens.
XX
PN    WO200065056-A2.
XX
PD    02-NOV-2000.
XX
PF    26-APR-2000; 2000WO-US011319.
XX
PR    26-APR-1999;   99US-0131051P.
XX
PA    (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI    Scharenberg AM;
XX
DR    WPI; 2000-687347/67.
```

```
  Query Match               100.0%;  Score 7950;  DB 3;  Length 1503;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1503;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy        1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60

Qy       61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120

Qy      121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180

Qy      181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240

Qy      241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300

Qy      301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA 360

Qy      361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420

Qy      421 EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK 480

Qy      481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540

Qy      541 VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ 600

Qy      601 GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660

Qy      661 ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720

Qy      721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780
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Qy    781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840

Qy    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900

Qy    901 LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE 960

Qy    961 RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF 1020

Qy   1021 PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA 1080

Qy   1081 PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ 1140

Qy   1141 KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA 1200

Qy   1201 SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE 1260

Qy   1261 KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ 1320

Qy   1321 AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP 1380

Qy   1381 LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI 1440

Qy   1441 ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG 1500

Qy   1501 AHY 1503
          |||
Db   1501 AHY 1503
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7950	100.0	1503	4	US-09-600-087-2	Sequence 2, Appli
2	2216	27.9	1095	4	US-09-636-215-780	Sequence 780, App
3	2216	27.9	1095	4	US-09-685-166A-780	Sequence 780, App
4	2212	27.8	1095	3	US-09-112-096-15	Sequence 15, Appl
5	2212	27.8	1095	4	US-09-636-215-778	Sequence 778, App
6	2212	27.8	1095	4	US-09-685-166A-778	Sequence 778, App
7	1423	17.9	1533	1	US-08-623-679-9	Sequence 9, Appli
8	1423	17.9	1533	3	US-08-933-774-9	Sequence 9, Appli
9	1423	17.9	1533	3	US-09-181-030-9	Sequence 9, Appli
10	1423	17.9	1533	4	US-09-534-242-9	Sequence 9, Appli
11	1423	17.9	1533	4	US-09-454-854-9	Sequence 9, Appli

RESULT 1
US-09-600-087-2
; Sequence 2, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
;   APPLICANT: Shimizu, No. 6548272uyoshi
;   APPLICANT: Nagamine, Kentaro
;   TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
;   FILE REFERENCE: 11283-004001
;   CURRENT APPLICATION NUMBER: US/09/600,087
;   CURRENT FILING DATE: 2000-07-11
;   PRIOR APPLICATION NUMBER: PCT/JP99/06289
;   PRIOR FILING DATE: 1999-11-11
;   PRIOR APPLICATION NUMBER: JP/321200/1998
;   PRIOR FILING DATE: 1998-11-12
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1503
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: TRANSMEM
;   LOCATION: (320)...(344)
;   NAME/KEY: TRANSMEM
;   LOCATION: (750)...(773)
;   NAME/KEY: TRANSMEM
;   LOCATION: (794)...(818)
;   NAME/KEY: TRANSMEM
;   LOCATION: (867)...(891)
;   NAME/KEY: TRANSMEM
;   LOCATION: (900)...(924)
;   NAME/KEY: TRANSMEM
;   LOCATION: (932)...(956)
;   NAME/KEY: TRANSMEM
;   LOCATION: (1024)...(1048)
US-09-600-087-2

  Query Match   100.0%; Score 7950; DB 4; Length 1503;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1503; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60

Qy   61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120

Qy   121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180

Qy   181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240

Qy   241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300

Qy   301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA 360

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Qy    361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420

Qy    421 EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 EGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK 480

Qy    481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540

Qy    541 VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLNVQ 600

Qy    601 GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660

Qy    661 ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720

Qy    721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780

Qy    781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840

Qy    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900

Qy    901 LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE 960

Qy    961 RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF 1020

Qy   1021 PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 PEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQVQEHTDQIWKFQRHDLIEEYHGRPAA 1080

Qy   1081 PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ 1140

Qy   1141 KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA 1200

Qy   1201 SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE 1260

Qy   1261 KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 KVPWETEFLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ 1320

Qy   1321 AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRRNEDGAICRKSIKKMLEVLVVKLP 1380

Qy   1381 LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1381 LSEHWALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKCGMEVYKGYMDDPRNTDNAWI 1440

Qy      1441 ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRRIPLYANHKTLLQKAAAEFG 1500

Qy      1501 AHY 1503
             |||
Db      1501 AHY 1503
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RESULT 2
US-09-636-215-780
; Sequence 780, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: Harlocker, Susan L.
;   APPLICANT: Jiang, Yuqui
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Retter, Marc W.
;   APPLICANT: Stolk, John A.
;   APPLICANT: Day, Craig H.
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Carter, Darrick
;   APPLICANT: Li, Samuel
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Hepler, William
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;   FILE REFERENCE: 210121.42717C17
;   CURRENT APPLICATION NUMBER: US/09/636,215
;   CURRENT FILING DATE: 2000-08-10
;   NUMBER OF SEQ ID NOS: 852
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 780
;   LENGTH: 1095
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1095)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-636-215-780

  Query Match   27.9%; Score 2216; DB 4; Length 1095;
  Best Local Similarity 41.2%; Pred. No. 4.6e-210;
  Matches 468; Conservative 208; Mismatches 353; Indels 108; Gaps   22;

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Qy        56 QESLSSWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQ--- 112
             :  |  ::|  |  ||:|||:|  : ||    | : ||:||| ||:|      |||
Db        29 ESDLVNFIQANFKKRECVFFTKDSK---ATENVCKCGYAQSQHME--------GTQINQ 76

Qy       113 ---WDPKKHVQEMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNL 169
                |: ||| :| |||||||| |   | :| ||:|:| || : ::| |:|||| | |||
Db        77 SEKWNYKKHTKEFPTDAFGDIQFETLGKK-GKYIRLSCDTDAEILYELLTQHWHLKTPNL 135

Qy       170 LISVTGGAKNFNMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSS 229
             :||||||||||| :|||:: || | |: :||: ||||:|||:| |:|| :|| ||| ::|
Db       136 VISVTGGAKNFALKPRMRKIFSR-LIYIAQSKGAWILTGGTHYGLMKYIGEVVRDNTISR 194

Qy       230 SYKEGELITIGVATWGTVHRREGLIH---PTGSFPAEYILDEDGQGNLTCLDSNHSHFIL 286
             | :|   :: ||:| ||| | |: ||      | |||:::|: : | ||:||:| :|
Db       195 SSEE-NIVAIGIAAWGMVSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLL 253

Qy       287 VDDGTHGQYGVEIPLRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTN 346
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```
               ||:| ||   ||   ||  :|||:|||:| :      ||||||   ||  || |: : |
Db     254 VDNGCHGHPTVEAKLRNQLEKYISERTIQDSNYGGKIPIVCFAQGGGKETLKAINTSIKN 313

Qy     347 GTPCVVVEGSGRVADVIAQVANLPVSD-ITISLIQQKLSVFFQEMFETFTESRIVEWTKK 405
               |||||||||::||||| :  : | |:| | :::|| |    |     | | |
Db     314 KIPCVVVEGSGQIADVIASL--VEVEDALTSSAVKEKLVRFLPRTVSRLPEEETESWIKW 371

Qy     406 IQDIVRRRQLLTVFREGKDGQQDVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRV 465
               ::::|:  |||| :  : | :| || || || :  :  :|| |||| : ||::
Db     372 LKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQ-DKDNWNGQLKLLLEWNQL 430

Qy     466 DIARSEIFMDEWQWKPSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYEN 525
               |:| ||| :: :|: :|| |   ||| ::|:||:|||||: |::|:| | | |: |
Db     431 DLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN 490

Qy     526 LDPSCLFHSKLQKVLVEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRHNDR 585
               | | : ||             |        : :|:: :| :    ||| |
Db     491 -HFSTLVYRNLQ--------------IAKNSYNDALLTFVWKLVANFRRGFRKEDR-NGR 534

Qy     586 LRLLLPVPHVKLNVQGVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQS 645
               : : :  ||           |   |:: | ||||:||::||: :|| |:
Db     535 -------DEMDIELHDVS-----------PITRHPLQALFIWAILQNKKELSKVIWEQT 575

Qy     646 QDCIAAALACSKILKELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQKLL 705
               : | ||| ||:||  |:| :|  | ::: |  || ||| ||: :||||| ||: |::||
Db     576 RGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLL 635

Qy     706 TRVSEAWGKTTCLQLALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPL 765
               |||| : ||:||:|:|| |  |:: :| ||:| |:|::| |  |:: ||:   ||
Db     636 VYSCEAWGGSNCLELAVEATDQHFIAQPGVQNFLSKQWYGEISRDTKNWKIILCLFIIPL 695

Qy     766 LLTGLISFREKRLQDVGTPAARAR-------AFFTAPVVVFHLNILSYFAFLCLFAYVLM 818
               :  | :|||:|         |  : :       ||||| ||| |:: | ||| |||||:
Db     696 VGCGFVSFRKK-------PVDKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLL 748

Qy     819 VDFQPVPSWCECAIYLWLFSLVCEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILL 878
               :||  ||    | :|  :| | |:|:|| : :          ||:| || :|    :
Db     749 MDFHSVPHPPELVLYSLVFVLFCDEVRQWYVN---------GVNYFTDLWNVMDTLGLFY 799

Qy     879 FVAGLTCRL---IPATLYPGRVILSLDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVF 935
               |:||: || :  ::|| |||| ||:|: ||:|| |||:||||:: ||||||:::|: |||
Db     800 FIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTVSRNLGPKIIMLQRMLIDVF 859

Qy     936 FFLFLLAVWVVSFGVAKQAILIHNERRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEH 995
               ||||| | |:|:|||||:| || ||:| |:|| |:|| :|| || :||:| :|| :: |
Db     860 FFLFLFAXWMVAFGVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDVDGTTYDFAH 919

Qy     996 CSPNGTDPYKPKCPESDATQQRPAFPEWLTVLLLCLYLLFTNILLLNLLIAMFNYTFQQV 1055
               |:  |  : || | | |     | ||||:|: |:|:|:| |||||:||:||| || |
Db     920 CTFTGNES-KPLCVELD-EHNLPRFPEWITIPLVCIYMLSTNILLVNLLVAMFGYTVGTV 977

Qy    1056 QEHTDQIWKFQRHDLIEEYHGRPAAPPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEK 1115
               ||: ||:||||: |::|| |  | | ||| ::  : :|:    ::: :       |
Db     978 QENNDQVWKFQRYFLVQEYCSRLNIPFPFIVFAYFYMVVKKCFKCCCKEKNMESSVCCFK 1037

Qy    1116 NEEAALLSWEIYLKENYLQNRQFQQKQRPEQK----------------IEDISNKV 1155
               ||:  |:||  :|||||      :   |:          :::|:||:
Db    1038 NEDNETLAWEGVMKENYLVKINTKANDTSEEMRHRFRQLDTKLNDLKGLLKEIANKI 1094
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```
                                  SUMMARIES
                          %
Result               Query
  No.    Score    Match  Length  DB   ID               Description
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     1    7950   100.0    1503    1   TRL2_HUMAN       O94759 homo sapien
     2  1282.5    16.1    2032    1   TRPG_CAEEL       Q93971 caenorhabdi
     3     659     8.3    1017    1   TRL3_HUMAN       Q9hcf6 homo sapien
     4     450     5.7    1418    1   CE11_CAEEL       P34641 caenorhabdi
     5   436.5     5.5     350    1   NUD9_HUMAN       Q9bw91 homo sapien
```

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     6    377.5    4.7     260   1   YQO8_CAEEL                    Q09297  caenorhabdi
     7    356      4.5    1027   1   TRPL_CAEEL                    P34586  caenorhabdi
     8    344      4.3    1124   1   TRPL_DROME                    P48994  drosophila
     9    341.5    4.3     975   1   TRP5_MOUSE                    Q9qx29  mus musculu
    10    340      4.3     973   1   TRP5_HUMAN                    Q9ul62  homo sapien
    11    334.5    4.2     974   1   TRP5_RABIT                    062852  oryctolagus
    12    331      4.2     885   1   TRP2_RAT                      Q9r283  rattus norv
    13    331      4.2     977   1   TRP4_HUMAN                    Q9ubn4  homo sapien
    14    324.5    4.1     981   1   TRP4_BOVIN                    P79100  bos taurus
    15    321.5    4.0    1275   1   TRP_DROME                     P19334  drosophila
    16    321      4.0     977   1   TRP4_RAT                      035119  rattus norv
```

RESULT 1
TRL2_HUMAN
```
ID   TRL2_HUMAN      STANDARD;      PRT;  1503 AA.
AC   O94759; Q96KN6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Long transient receptor potential channel 2 (LTrpC2) (Transient
DE   receptor potential channel 7) (TrpC7).
GN   TRPM2 OR LTRPC2 OR TRPC7 OR KNP3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=99026133; PubMed=9806837;
RA   Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F.,
RA   Shimizu N.;
RT   "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)
RT   highly expressed in brain.";
RL   Genomics 54:124-131(1998).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=22075135; PubMed=11960981;
RA   Wehage E., Eisfeld J., Heiner I., Jungling E., Zitt C., Luckhoff A.;
RT   "Activation of the cation channel long transient receptor potential
RT   channel 2 (LTRPC2) by hydrogen peroxide. A splice variant reveals a
RT   mode of activation independent of ADP-ribose.";
RL   J. Biol. Chem. 277:23150-23156(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20289799; PubMed=10830953;
RA   Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA   Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA   Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA   Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA   Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA   Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA   Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA   Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA   Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA   Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA   Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA   Lehrach H., Reinhardt R., Yaspo M.-L.;
RT   "The DNA sequence of human chromosome 21.";
RL   Nature 405:311-319(2000).
CC   -!- FUNCTION: May be a calcium channel.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=O94759-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O94759-2; Sequence=VSP_006574, VSP_006575;
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain.
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CC   -!- SIMILARITY: Belongs to the transient receptor family. LTrpC
CC       subfamily.
CC   ----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------
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DR   EMBL; AJ417076; CAD01139.1; -.
DR   EMBL; AP001754; BAA95563.1; -.
DR   Genew; HGNC:12339; TRPM2.
DR   MIM; 603749; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005262; F:calcium channel activity; TAS.
DR   GO; GO:0006816; P:calcium ion transport; TAS.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR002153; Trans_receptor.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01097; TRNSRECEPTRP.
KW   Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW   Alternative splicing.
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FT   TRANSMEM   753    773       POTENTIAL.
FT   DOMAIN     774    795       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   796    816       POTENTIAL.
FT   DOMAIN     817    820       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   821    841       POTENTIAL.
FT   DOMAIN     842    896       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   897    917       POTENTIAL.
FT   DOMAIN     918    936       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   937    957       POTENTIAL.
FT   DOMAIN     958   1025       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM  1026   1046       POTENTIAL.
FT   DOMAIN    1047   1503       CYTOPLASMIC (POTENTIAL).
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FT                              (in isoform 2).
FT                              /FTId=VSP_006575.
FT   CONFLICT  1088   1088       S -> N (IN REF. 2).
FT   CONFLICT  1189   1189       R -> Q (IN REF. 3).
SQ   SEQUENCE   1503 AA;  171225 MW;  AD329AE79F1A71B5 CRC64;

   Query Match           100.0%;  Score 7950;  DB 1;  Length 1503;
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   Matches 1503;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       61 SWIPENIKKKECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120
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Qy      121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180
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Db      121 EMPTDAFGDIVFTGLSQKVKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180

Qy      181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240

Qy      241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVEIP 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420
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Qy    481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540
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Qy    721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCMLAFPLLLTGLISFREKRLQD 780
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Qy    781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV 840

Qy    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
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          .||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    961 RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF 1020
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Qy   1141 KQRPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA 1200
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Qy   1201 SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE 1260
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SEQ ID NO: 2

SUMMARIES

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8	3220	71.4	5980	10	MMU344343	AJ344343 Mus muscu
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DEFINITION   Sequence 5 from Patent WO0065056.
ACCESSION    AX042216
VERSION      AX042216.1  GI:11340930
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Scharenberg,A.M.
  TITLE      Nucleic acids encoding a mutt domain-containing polypeptide
  JOURNAL    Patent: WO 0065056-A 5 02-NOV-2000;
             Beth Israel Deaconess Medical Center, Inc. (US)
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          ORIGIN

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      Qy       421 AAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAGCGTGATCTACCACCTCATGACCCAG 480
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      Qy       541 AACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAGAGGCCTGGTCAAGGTGGCTCAGACC 600
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Qy      901 CTGAGGACCAGGCTGGAGAAGTTCATATCGGAGCAGACCAAGGAAAGAGGAGGTGTGGCC 960
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Qy     1021 GACAACGCCACCACCAACGGCACCCCCTGTGTGGTTGTGGAGGGCTCGGGCCGCGTGGCC 1080
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Qy     1081 GACGTCATTGCCCAGGTGGCCAACCTGCCTGTCTCGGACATCACTATCTCCCTGATCCAG 1140
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Db     1526 GACGTCATTGCCCAGGTGGCCAACCTGCCTGTCTCGGACATCACTATCTCCCTGATCCAG 1585

Qy     1141 CAGAAACTGAGCGTGTTCTTCCAGGAGATGTTTGAGACCTTCACGGAAAGCAGGATTGTC 1200
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Qy     1201 GAGTGGACCAAAAAGATCCAAGATATTGTCCGGAGGCGGCAGCTGCTGACTGTCTTCCGG 1260
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Qy     1261 GAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGCCATCTTGCAGGCCTTGCTGAAAGCC 1320
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Db     1706 GAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGCCATCTTGCAGGCCTTGCTGAAAGCC 1765

Qy     1321 TCACGGAGCCAAGACCACTTTGGCCACGAGAACTGGGACCACCAGCTGAAACTGGCAGTG 1380
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Qy      2041  GAGTATGAGCACAGAGCCATCGGGGTCTTCACCGAGTGCTACCGGAAGGACGAAGAGAGA  2100
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Qy      2221  AAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGGGCTGTGGCGTGTGACCCTGTGCATG  2280
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RESULT 6
AB001535
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DEFINITION  Homo sapiens mRNA, complete cds.
ACCESSION   AB001535
VERSION     AB001535.1  GI:3928755
KEYWORDS    KNP3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Nagamine,K., Kudoh,J., Minoshima,S., Kawasaki,K., Asakawa,S.,
            Ito,F. and Shimizu,N.
  TITLE     Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)
            highly expressed in brain
  JOURNAL   Genomics 54 (1), 124-131 (1998)
  MEDLINE   99026133
   PUBMED   9806837
REFERENCE   2  (bases 1 to 6220)
  AUTHORS   Shimizu,N.
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ORIGIN

    Query Match   100.0%; Score 4512; DB 9; Length 6220;
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Db    566   TTCAAGAGCTGGAGGCTACAGTGCCCCTTCGGCAACAATGACAAGCAAGAAAGCCTCAGT   625

Qy    181   TCGTGGATTCCTGAAAACATCAAGAAGAAAGAATGCGTGTATTTTGTGGAAAGTTCCAAA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    626   TCGTGGATTCCTGAAAACATCAAGAAGAAAGAATGCGTGTATTTTGTGGAAAGTTCCAAA   685

Qy    241   CTGTCTGATGCTGGGAAGGTGGTGTGTCAGTGTGGCTACACGCATGAGCAGCACTTGGAG   300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    686   CTGTCTGATGCTGGGAAGGTGGTGTGTCAGTGTGGCTACACGCATGAGCAGCACTTGGAG   745

Qy    301   GAGGCTACCAAGCCCCACACCTTCCAGGGCACACAGTGGGACCCAAAGAAACATGTCCAG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    746   GAGGCTACCAAGCCCCACACCTTCCAGGGCACACAGTGGGACCCAAAGAAACATGTCCAG   805

Qy    361   GAGATGCCAACCGATGCCTTTGGCGACATCGTCTTCACGGGCCTGAGCCAGAAGGTGAAA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    806   GAGATGCCAACCGATGCCTTTGGCGACATCGTCTTCACGGGCCTGAGCCAGAAGGTGAAA   865

Qy    421   AAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAGCGTGATCTACCACCTCATGACCCAG   480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    866   AAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAGCGTGATCTACCACCTCATGACCCAG   925

Qy    481   CACTGGGGGCTGGACGTCCCCAATCTCTTGATCTCGGTGACCGGGGGGGCCAAGAACTTC   540
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    926   CACTGGGGGCTGGACGTCCCCAATCTCTTGATCTCGGTGACCGGGGGGGGCCAAGAACTTC   985

Qy    541   AACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAGAGGCCTGGTCAAGGTGGCTCAGACC   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    986   AACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAGAGGCCTGGTCAAGGTGGCTCAGACC   1045

Qy    601   ACAGGGGCCTGGATCATCACAGGGGGGTCCCACACCGGCGTCATGAAGCAGGTAGGCGAG   660
            |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1046  ACAGGGGCCTGGATCATCACAGGGGGGTCCCACACCGGCGTCATGAAGCAGGTAGGCGAG   1105

Qy    661   GCGGTGCGGGACTTCAGCCTGAGCAGCAGCTACAAGGAAGGCGAGCTCATCACCATCGGA   720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1106  GCGGTGCGGGACTTCAGCCTGAGCAGCAGCTACAAGGAAGGCGAGCTCATCACCATCGGA   1165

Qy    721   GTCGCCACCTGGGGCACTGTCCACCGCCGCGAGGGCCTGATCCATCCCACGGGCAGCTTC   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1166  GTCGCCACCTGGGGCACTGTCCACCGCCGCGAGGGCCTGATCCATCCCACGGGCAGCTTC   1225

Qy    781   CCCGCCGAGTACATACTGGATGAGGATGGCCAAGGGAACCTGACCTGCCTAGACAGCAAC   840
            ||||| |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    1226  CCCGCCGAGTACATACTGGATGAGGATGGCCAAGGGAACCTGACCTGCCTAGACAGCAAC   1285

Qy    841   CACTCTCACTTCATCCTCGTGGACGACGGGACCCACGGCCAGTACGGGGTGGAGATTCCT   900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1286  CACTCTCACTTCATCCTCGTGGACGACGGGACCCACGGCCAGTACGGGGTGGAGATTCCT   1345

Qy    901   CTGAGGACCAGGCTGGAGAAGTTCATATCGGAGCAGACCAAGGAAAGAGGAGGTGTGGCC   960
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    1346  CTGAGGACCAGGCTGGAGAAGTTCATATCGGAGCAGACCAAGGAAAGAGGAGGTGTGGCC   1405

Qy    961   ATCAAGATCCCCATCGTGTGCGTGGTGCTGGAGGGCGGCCCGGGCACGTTGCACACCATC   1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1406  ATCAAGATCCCCATCGTGTGCGTGGTGCTGGAGGGCGGCCCGGGCACGTTGCACACCATC   1465

Qy    1021  GACAACGCCACCACCAACGGCACCCCCTGTGTGGTTGTGGAGGGCTCGGGCCGCGTGGCC   1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1466  GACAACGCCACCACCAACGGCACCCCCTGTGTGGTTGTGGAGGGCTCGGGCCGCGTGGCC   1525

Qy    1081  GACGTCATTGCCCAGGTGGCCAACCTGCCTGTCTCGGACATCACTATCTCCCTGATCCAG   1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1526  GACGTCATTGCCCAGGTGGCCAACCTGCCTGTCTCGGACATCACTATCTCCCTGATCCAG   1585

Qy    1141  CAGAAACTGAGCGTGTTCTTCCAGGAGATGTTTGAGACCTTCACGGAAAGCAGGATTGTC   1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1586  CAGAAACTGAGCGTGTTCTTCCAGGAGATGTTTGAGACCTTCACGGAAAGCAGGATTGTC   1645

Qy    1201  GAGTGGACCAAAAAGATCCAAGATATTGTCCGGAGGCGGCAGCTGCTGACTGTCTTCCGG   1260
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            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1646  GAGTGGACCAAAAAGATCCAAGATATTGTCCGGAGGCGGCAGCTGCTGACTGTCTTCCGG 1705

Qy    1261  GAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGCCATCTTGCAGGCCTTGCTGAAAGCC 1320
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1706  GAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGCCATCTTGCAGGCCTTGCTGAAAGCC 1765

Qy    1321  TCACGGAGCCAAGACCACTTTGGCCACGAGAACTGGGACCACCAGCTGAAACTGGCAGTG 1380
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1766  TCACGGAGCCAAGACCACTTTGGCCACGAGAACTGGGACCACCAGCTGAAACTGGCAGTG 1825

Qy    1381  GCATGGAATCGCGTGGACATTGCCCGCAGTGAGATCTTCATGGATGAGTGGCAGTGGAAG 1440
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1826  GCATGGAATCGCGTGGACATTGCCCGCAGTGAGATCTTCATGGATGAGTGGCAGTGGAAG 1885

Qy    1441  CCTTCAGATCTGCACCCCACGATGACAGCTGCACTCATCTCCAACAAGCCTGAGTTTGTG 1500
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1886  CCTTCAGATCTGCACCCCACGATGACAGCTGCACTCATCTCCAACAAGCCTGAGTTTGTG 1945

Qy    1501  AAGCTCTTCCTGGAAAACGGGGTGCAGCTGAAGGAGTTTGTCACCTGGGACACCTTGCTC 1560
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1946  AAGCTCTTCCTGGAAAACGGGGTGCAGCTGAAGGAGTTTGTCACCTGGGACACCTTGCTC 2005

Qy    1561  TACCTGTACGAGAACCTGGACCCCTCCTGCCTGTTCCACAGCAAGCTGCAAAAGGTGCTG 1620
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2006  TACCTGTACGAGAACCTGGACCCCTCCTGCCTGTTCCACAGCAAGCTGCAAAAGGTGCTG 2065

Qy    1621  GTGGAGGATCCCGAGCGCCCGGCTTGCGCGCCCGCGGCGCCCCGCCTGCAGATGCACCAC 1680
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2066  GTGGAGGATCCCGAGCGCCCGGCTTGCGCGCCCGCGGCGCCCCGCCTGCAGATGCACCAC 2125

Qy    1681  GTGGCCCAGGTGCTGCGGGAGCTGCTGGGGGACTTCACGCAGCCGCTTTATCCCCGGCCC 1740
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2126  GTGGCCCAGGTGCTGCGGGAGCTGCTGGGGGACTTCACGCAGCCGCTTTATCCCCGGCCC 2185

Qy    1741  CGGCACAACGACCGGCTGCGGCTCCTGCTGCCCGTTCCCCACGTCAAGCTCAACGTGCAG 1800
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2186  CGGCACAACGACCGGCTGCGGCTCCTGCTGCCCGTTCCCCACGTCAAGCTCAACGTGCAG 2245

Qy    1801  GGAGTGAGCCTCCGGTCCCTCTACAAGCGTTCCTCAGGCCATGTGACCTTCACCATGGAC 1860
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2246  GGAGTGAGCCTCCGGTCCCTCTACAAGCGTTCCTCAGGCCATGTGACCTTCACCATGGAC 2305

Qy    1861  CCCATCCGTGACCTTCTCATTTGGGCCATTGTCCAGAACCGTCGGGAGCTGGCAGGAATC 1920
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2306  CCCATCCGTGACCTTCTCATTTGGGCCATTGTCCAGAACCGTCGGGAGCTGGCAGGAATC 2365

Qy    1921  ATCTGGGCTCAGAGCCAGGACTGCATCGCAGCGGCCTTGGCCTGCAGCAAGATCCTGAAG 1980
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2366  ATCTGGGCTCAGAGCCAGGACTGCATCGCAGCGGCCTTGGCCTGCAGCAAGATCCTGAAG 2425

Qy    1981  GAACTGTCCAAGGAGGAGGAGGACACGGACAGCTCGGAGGAGATGCTGGCGCTGGCGGAG 2040
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2426  GAACTGTCCAAGGAGGAGGAGGACACGGACAGCTCGGAGGAGATGCTGGCGCTGGCGGAG 2485

Qy    2041  GAGTATGAGCACAGAGCCATCGGGGTCTTCACCGAGTGCTACCGGAAGGACGAAGAGAGA 2100
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2486  GAGTATGAGCACAGAGCCATCGGGGTCTTCACCGAGTGCTACCGGAAGGACGAAGAGAGA 2545

Qy    2101  GCCCAGAAACTGCTCACCCGCGTGTCCGAGGCCTGGGGGAAGACCACCTGCCTGCAGCTC 2160
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2546  GCCCAGAAACTGCTCACCCGCGTGTCCGAGGCCTGGGGGAAGACCACCTGCCTGCAGCTC 2605

Qy    2161  GCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTCACGGGGGCATCCAGGCCTTCCTGACC 2220
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2606  GCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTCACGGGGGCATCCAGGCCTTCCTGACC 2665

Qy    2221  AAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGGGCTGTGGCGTGTGACCCTGTGCATG 2280
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2666  AAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGGGCTGTGGCGTGTGACCCTGTGCATG 2725
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Qy   2281 CTGGCCTTCCCGCTGCTCCTCACCGGCCTCATCTCCTTCAGGGAGAAGAGGCTGCAGGAT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2726 CTGGCCTTCCCGCTGCTCCTCACCGGCCTCATCTCCTTCAGGGAGAAGAGGCTGCAGGAT 2785

Qy   2341 GTGGGCACCCCCGCGGCCCGCGCCCGTGCCTTCTTCACCGCACCCGTGGTGGTCTTCCAC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2786 GTGGGCACCCCCGCGGCCCGCGCCCGTGCCTTCTTCACCGCACCCGTGGTGGTCTTCCAC 2845

Qy   2401 CTGAACATCCTCTCCTACTTCGCCTTCCTCTGCCTGTTCGCCTACGTGCTCATGGTGGAC 2460
          |||||||||||||||||||||||||||||||||||||!|||||||||||||||||||||
Db   2846 CTGAACATCCTCTCCTACTTCGCCTTCCTCTGCCTGTTCGCCTACGTGCTCATGGTGGAC 2905

Qy   2461 TTCCAGCCTGTGCCCTCCTGGTGCGAGTGTGCCATCTACCTCTGGCTCTTCTCCTTGGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906 TTCCAGCCTGTGCCCTCCTGGTGCGAGTGTGCCATCTACCTCTGGCTCTTCTCCTTGGTG 2965

Qy   2521 TGCGAGGAGATGCGGCAGCTCTTCTATGACCCTGACGAGTGCGGGCTGATGAAGAAGGCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2966 TGCGAGGAGATGCGGCAGCTCTTCTATGACCCTGACGAGTGCGGGCTGATGAAGAAGGCA 3025

Qy   2581 GCCTTGTACTTCAGTGACTTCTGGAATAAGCTGGACGTCGGCGCAATCTTGCTCTTCGTG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3026 GCCTTGTACTTCAGTGACTTCTGGAATAAGCTGGACGTCGGCGCAATCTTGCTCTTCGTG 3085

Qy   2641 GCAGGGCTGACCTGCAGGCTCATCCCGGCGACGCTGTACCCCGGGCGCGTCATCCTCTCT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3086 GCAGGGCTGACCTGCAGGCTCATCCCGGCGACGCTGTACCCCGGGCGCGTCATCCTCTCT 3145

Qy   2701 CTGGACTTCATCCTGTTCTGCCTCCGGCTCATGCACATTTTTACCATCAGTAAGACGCTG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3146 CTGGACTTCATCCTGTTCTGCCTCCGGCTCATGCACATTTTTACCATCAGTAAGACGCTG 3205

Qy   2761 GGGCCCAAGATCATCATTGTGAAGCGGATGATGAAGGACGTCTTCTTCTTCCTCTTCCTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3206 GGGCCCAAGATCATCATTGTGAAGCGGATGATGAAGGACGTCTTCTTCTTCCTCTTCCTG 3265

Qy   2821 CTGGCTGTGTGGGTGGTGTCCTTCGGGGTGGCCAAGCAGGCCATCCTCATCCACAACGAG 2880
          ||||!|||||||||||||||||||||||||||||||||!||||||||||||||||||||
Db   3266 CTGGCTGTGTGGGTGGTGTCCTTCGGGGTGGCCAAGCAGGCCATCCTCATCCACAACGAG 3325

Qy   2881 CGCCGGGTGGACTGGCTGTTCCGAGGGGCCGTCTACCACTCCTACCTCACCATCTTCGGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3326 CGCCGGGTGGACTGGCTGTTCCGAGGGGCCGTCTACCACTCCTACCTCACCATCTTCGGG 3385

Qy   2941 CAGATCCCGGGCTACATCGACGGTGTGAACTTCAACCCGGAGCACTGCAGCCCCAATGGC 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3386 CAGATCCCGGGCTACATCGACGGTGTGAACTTCAACCCGGAGCACTGCAGCCCCAATGGC 3445

Qy   3001 ACCGACCCCTACAAGCCTAAGTGCCCCGAGAGCGACGCGACGCAGCAGAGGCCGGCCTTC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3446 ACCGACCCCTACAAGCCTAAGTGCCCCGAGAGCGACGCGACGCAGCAGAGGCCGGCCTTC 3505

Qy   3061 CCTGAGTGGCTGACGGTCCTCCTACTCTGCCTCTACCTGCTCTTCACCAACATCCTGCTG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3506 CCTGAGTGGCTGACGGTCCTCCTACTCTGCCTCTACCTGCTCTTCACCAACATCCTGCTG 3565

Qy   3121 CTCAACCTCCTCATCGCCATGTTCAACTACACCTTCCAGCAGGTGCAGGAGCACACGGAC 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3566 CTCAACCTCCTCATCGCCATGTTCAACTACACCTTCCAGCAGGTGCAGGAGCACACGGAC 3625

Qy   3181 CAGATTTGGAAGTTCCAGCGCCATGACCTGATCGAGGAGTACCACGGCCGCCCCGCCGCG 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3626 CAGATTTGGAAGTTCCAGCGCCATGACCTGATCGAGGAGTACCACGGCCGCCCCGCCGCG 3685

Qy   3241 CCGCCCCCTTCATCCTCCTCAGCCACCTGCAGCTCTTCATCAAGAGGGTGGTCCTGAAG 3300
          ||||||||||||||||||||||||||!|||||||||||||||||||||||||||||||
Db   3686 CCGCCCCCCTTCATCCTCCTCAGCCACCTGCAGCTCTTCATCAAGAGGGTGGTCCTGAAG 3745

Qy   3301 ACTCCGGCCAAGAGGCACAAGCAGCTCAAGAACAAGCTGGAGAAGAACGAGGAGGCGGCC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3746 ACTCCGGCCAAGAGGCACAAGCAGCTCAAGAACAAGCTGGAGAAGAACGAGGAGGCGGCC 3805
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Qy    3361 CTGCTATCCTGGGAGATCTACCTGAAGGAGAACTACCTCCAGAACCGACAGTTCCAGCAA 3420
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Db    3806 CTGCTATCCTGGGAGATCTACCTGAAGGAGAACTACCTCCAGAACCGACAGTTCCAGCAA 3865

Qy    3421 AAGCAGCGGCCCGAGCAGAAGATCGAGGACATCAGCAATAAGGTTGACGCCATGGTGGAC 3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3866 AAGCAGCGGCCCGAGCAGAAGATCGAGGACATCAGCAATAAGGTTGACGCCATGGTGGAC 3925

Qy    3481 CTGCTGGACCTGGACCCACTGAAGAGGTCGGGCTCCATGGAGCAGAGGTTGGCCTCCCTG 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3926 CTGCTGGACCTGGACCCACTGAAGAGGTCGGGCTCCATGGAGCAGAGGTTGGCCTCCCTG 3985

Qy    3541 GAGGAGCAGGTGGCCCAGACAGCCCGAGCCCTGCACTGGATCGTGAGGACGCTGCGGGCC 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3986 GAGGAGCAGGTGGCCCAGACAGCCCGAGCCCTGCACTGGATCGTGAGGACGCTGCGGGCC 4045

Qy    3601 AGCGGCTTCAGCTCGGAGGCGGACGTCCCCACTCTGGCCTCCCAGAAGGCCGCGGAGGAG 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4046 AGCGGCTTCAGCTCGGAGGCGGACGTCCCCACTCTGGCCTCCCAGAAGGCCGCGGAGGAG 4105

Qy    3661 CCGGATGCTGAGCCGGGAGGCAGGAAGAAGACGGAGGAGCCGGGCGACAGCTACCACGTG 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4106 CCGGATGCTGAGCCGGGAGGCAGGAAGAAGACGGAGGAGCCGGGCGACAGCTACCACGTG 4165

Qy    3721 AATGCCCGGCACCTCCTCTACCCCAACTGCCCTGTCACGCGCTTCCCCGTGCCCAACGAG 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4166 AATGCCCGGCACCTCCTCTACCCCAACTGCCCTGTCACGCGCTTCCCCGTGCCCAACGAG 4225

Qy    3781 AAGGTGCCCTGGGAGACGGAGTTCCTGATCTATGACCCACCCTTTTACACGGCAGAGAGG 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4226 AAGGTGCCCTGGGAGACGGAGTTCCTGATCTATGACCCACCCTTTTACACGGCAGAGAGG 4285

Qy    3841 AAGGACGCGGCCGCCATGGACCCCATGGGAGACACCCTGGAGCCACTGTCCACGATCCAG 3900
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Qy    3901 TACAACGTGGTGGATGGCCTGAGGGACCGCCGGAGCTTCCACGGGCCGTACACAGTGCAG 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4346 TACAACGTGGTGGATGGCCTGAGGGACCGCCGGAGCTTCCACGGGCCGTACACAGTGCAG 4405

Qy    3961 GCCGGGTTGCCCCTGAACCCCATGGGCCGCACAGGACTGCGTGGGCGCGGGAGCCTCAGC 4020
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Qy    4021 TGCTTCGGACCCAACCACACGCTGTACCCCATGGTCACGCGGTGGAGGCGGAACGAGGAT 4080
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Qy    4081 GGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCTGGAAGTGCTGGTGGTGAAGCTCCCT 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4526 GGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCTGGAAGTGCTGGTGGTGAAGCTCCCT 4585

Qy    4141 CTCTCCGAGCACTGGGCCCTGCCTGGGGGCTCCCGGGAGCCAGGGGAGATGCTACCTCGG 4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    4201 AAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCCGTCTTTTGAAAACTTGCTGAAGTGC 4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4646 AAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCCGTCTTTTGAAAACTTGCTGAAGTGC 4705

Qy    4261 GGCATGGAGGTGTACAAAGGCTACATGGATGACCCGAGGAACACGGACAATGCCTGGATC 4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    4381 AACTCTAACCTGCACGCCTGCGACTCGGGGGCCTCCATCCGATGGCAGGTGGTGGACAGG 4440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    4826 AACTCTAACCTGCACGCCTGCGACTCGGGGGCCTCCATCCGATGGCAGGTGGTGGACAGG 4885

Qy    4441 CGCATCCCACTCTATGCGAACCACAAGACCCTCCTCCAGAAGGCAGCCGCTGAGTTCGGG 4500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4886 CGCATCCCACTCTATGCGAACCACAAGACCCTCCTCCAGAAGGCAGCCGCTGAGTTCGGG 4945

Qy    4501 GCTCACTACTGA 4512
           ||||||||||||
Db    4946 GCTCACTACTGA 4957
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SUMMARIES

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                      %
Result           Query
   No.   Score  Match Length DB  ID                     Description
      -----------------------------------------------------------------------------
      1    4512  100.0   6220  4  US-09-600-087-1        Sequence 1, Appli
      2    611.6  13.6   3639  4  US-09-636-215-779      Sequence 779, App
      3    611.6  13.6   3639  4  US-09-685-166A-779     Sequence 779, App
      4    607.2  13.5   5668  3  US-09-112-096-14       Sequence 14, Appl
      5    607.2  13.5   5668  4  US-09-636-215-777      Sequence 777, App
      6    607.2  13.5   5668  4  US-09-685-166A-777     Sequence 777, App
      7    379.8   8.4   3848  3  US-09-112-096-28       Sequence 28, Appl
      8    306     6.8   1959  4  US-09-636-215-817      Sequence 817, App
      9    306     6.8   1959  4  US-09-685-166A-817     Sequence 817, App
     10    302.8   6.7   1690  3  US-09-112-096-27       Sequence 27, Appl
     11    250.2   5.5   1512  4  US-09-461-325-54       Sequence 54, Appl
     12    250.2   5.5   1512  4  US-10-012-542-54       Sequence 54, Appl
     13    244.8   5.4   1524  3  US-09-020-956-109      Sequence 109, App
     14    244.8   5.4   1524  3  US-09-030-607-109      Sequence 109, App
     15    244.8   5.4   1524  4  US-09-439-313-109      Sequence 109, App
     16    244.8   5.4   1524  4  US-09-352-616A-109     Sequence 109, App
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RESULT 1
US-09-600-087-1
.; Sequence 1, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
;   APPLICANT: Shimizu, No. 6548272uyoshi
;   APPLICANT: Nagamine, Kentaro
;   TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
;   FILE REFERENCE: 11283-004001
;   CURRENT APPLICATION NUMBER: US/09/600,087
;   CURRENT FILING DATE: 2000-07-11
;   PRIOR APPLICATION NUMBER: PCT/JP99/06289
;   PRIOR FILING DATE: 1999-11-11
;   PRIOR APPLICATION NUMBER: JP/321200/1998
;   PRIOR FILING DATE: 1998-11-12
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6220
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (446)...(4954)
;   NAME/KEY: polyA_signal
;   LOCATION: (5812)...(5817)
US-09-600-087-1

  Query Match   100.0%; Score 4512; DB 4; Length 6220;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 4512; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy       1 ATGGAGCCCTCAGCCCTGAGGAAAGCTGGCTCGGAGCAGGAGGAGGGCTTTGAGGGGCTG 60
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Db     446 ATGGAGCCCTCAGCCCTGAGGAAAGCTGGCTCGGAGCAGGAGGAGGGCTTTGAGGGGCTG 505
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Qy        61  CCCAGAAGGGTCACTGACCTGGGGATGGTCTCCAATCTCCGGCGCAGCAACAGCAGCCTC  120
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Db       506  CCCAGAAGGGTCACTGACCTGGGGATGGTCTCCAATCTCCGGCGCAGCAACAGCAGCCTC  565

Qy       121  TTCAAGAGCTGGAGGCTACAGTGCCCCTTCGGCAACAATGACAAGCAAGAAAGCCTCAGT  180
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Db       566  TTCAAGAGCTGGAGGCTACAGTGCCCCTTCGGCAACAATGACAAGCAAGAAAGCCTCAGT  625

Qy       181  TCGTGGATTCCTGAAAACATCAAGAAGAAAGAATGCGTGTATTTTGTGGAAAGTTCCAAA  240
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Db       626  TCGTGGATTCCTGAAAACATCAAGAAGAAAGAATGCGTGTATTTTGTGGAAAGTTCCAAA  685

Qy       241  CTGTCTGATGCTGGGAAGGTGGTGTGTCAGTGTGGCTACACGCATGAGCAGCACTTGGAG  300
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Db       686  CTGTCTGATGCTGGGAAGGTGGTGTGTCAGTGTGGCTACACGCATGAGCAGCACTTGGAG  745

Qy       301  GAGGCTACCAAGCCCCACACCTTCCAGGGCACACAGTGGGACCCAAAGAAACATGTCCAG  360
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Qy       361  GAGATGCCAACCGATGCCTTTGGCGACATCGTCTTCACGGGCCTGAGCCAGAAGGTGAAA  420
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Qy       421  AAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAGCGTGATCTACCACCTCATGACCCAG  480
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Db       866  AAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAGCGTGATCTACCACCTCATGACCCAG  925

Qy       481  CACTGGGGGCTGGACGTCCCCAATCTCTTGATCTCGGTGACCGGGGGGGCCAAGAACTTC  540
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Db       926  CACTGGGGGCTGGACGTCCCCAATCTCTTGATCTCGGTGACCGGGGGGGCCAAGAACTTC  985

Qy       541  AACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAGAGGCCTGGTCAAGGTGGCTCAGACC  600
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Db       986  AACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAGAGGCCTGGTCAAGGTGGCTCAGACC  1045

Qy       601  ACAGGGGCCTGGATCATCACAGGGGGGGTCCCACACCGGCGTCATGAAGCAGGTAGGCGAG  660
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Qy       661  GCGGTGCGGGACTTCAGCCTGAGCAGCAGCTACAAGGAAGGCGAGCTCATCACCATCGGA  720
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Db      1106  GCGGTGCGGGACTTCAGCCTGAGCAGCAGCTACAAGGAAGGCGAGCTCATCACCATCGGA  1165

Qy       721  GTCGCCACCTGGGGCACTGTCCACCGCCGCGAGGGCCTGATCCATCCCACGGGCAGCTTC  780
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Db      1166  GTCGCCACCTGGGGCACTGTCCACCGCCGCGAGGGCCTGATCCATCCCACGGGCAGCTTC  1225

Qy       781  CCCGCCGAGTACATACTGGATGAGGATGGCCAAGGGAACCTGACCTGCCTAGACAGCAAC  840
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Db      1226  CCCGCCGAGTACATACTGGATGAGGATGGCCAAGGGAACCTGACCTGCCTAGACAGCAAC  1285

Qy       841  CACTCTCACTTCATCCTCGTGGACGACGGGACCCACGGCCAGTACGGGGTGGAGATTCCT  900
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Db      1285  CACTCTCACTTCATCCTCGTGGACGACGGGACCCACGGCCAGTACGGGGTGGAGATTCCT  1345

Qy       901  CTGAGGACCAGGCTGGAGAAGTTCATATCGGAGCAGACCAAGGAAAGAGGAGGTGTGGCC  960
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Qy       961  ATCAAGATCCCCATCGTGTGCGTGGTGCTGGAGGGCGGCCCGGGCACGTTGCACACCATC  1020
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Qy      1021  GACAACGCCACCACCAACGGCACCCCCTGTGTGGTTGTGGAGGGCTCGGGCCGCGTGGCC  1080
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Qy      1141 CAGAAACTGAGCGTGTTCTTCCAGGAGATGTTTGAGACCTTCACGGAAAGCAGGATTGTC 1200
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Db      1646 GAGTGGACCAAAAAGATCCAAGATATTGTCCGGAGGCGGCAGCTGCTGACTGTCTTCCGG 1705

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Db      1706 GAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGCCATCTTGCAGGCCTTGCTGAAAGCC 1765

Qy      1321 TCACGGAGCCAAGACCACTTTGGCCACGAGAACTGGGACCACCAGCTGAAACTGGCAGTG 1380
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Qy      1381 GCATGGAATCGCGTGGACATTGCCCGCAGTGAGATCTTCATGGATGAGTGGCAGTGGAAG 1440
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Qy      1441 CCTTCAGATCTGCACCCCACGATGACAGCTGCACTCATCTCCAACAAGCCTGAGTTTGTG 1500
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Qy      1501 AAGCTCTTCCTGGAAAACGGGGTGCAGCTGAAGGAGTTTGTCACCTGGGACACCTTGCTC 1560
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Qy      1561 TACCTGTACGAGAACCTGGACCCCTCCTGCCTGTTCCACAGCAAGCTGCAAAAGGTGCTG 1620
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Qy      1621 GTGGAGGATCCCGAGCGCCCGGCTTGCGCGCCCGCGGCGCCCCGCCTGCAGATGCACCAC 1680
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Qy      1631 GTGGCCCAGGTGCTGCGGGAGCTGCTGGGGGACTTCACGCAGCCGCTTTATCCCCGGCCC 1740
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Qy      2041 GAGTATGAGCACAGAGCCATCGGGGTCTTCACCGAGTGCTACCGGAAGGACGAAGAGAGA 2100
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Db    2606 GCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTCACGGGGGCATCCAGGCCTTCCTGACC 2665

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Qy    2821 CTGGCTGTGTGGGTGGTGTCCTTCGGGGTGGCCAAGCAGGCCATCCTCATCCACAACGAG 2880
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Qy    2881 CGCCGGGTGGACTGGCTGTTCCGAGGGGCCGTCTACCACTCCTACCTCACCATCTTCGGG 2940
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Qy    3181 CAGATTTGGAAGTTCCAGCGCCATGACCTGATCGAGGAGTACCACGGCCGCCCCGCCGCG 3240
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Qy     4081 GGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCTGGAAGTGCTGGTGGTGAAGCTCCCT 4140
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Db     4526 GGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCTGGAAGTGCTGGTGGTGAAGCTCCCT 4585

Qy     4141 CTCTCCGAGCACTGGGCCCTGCCTGGGGGCTCCCGGGAGCCAGGGGAGATGCTACCTCGG 4200
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4586 CTCTCCGAGCACTGGGCCCTGCCTGGGGGCTCCCGGGAGCCAGGGGAGATGCTACCTCGG 4645

Qy     4201 AAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCCGTCTTTTGAAAACTTGCTGAAGTGC 4260
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4646 AAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCCGTCTTTTGAAAACTTGCTGAAGTGC 4705

Qy     4261 GGCATGGAGGTGTACAAAGGCTACATGGATGACCCGAGGAACACGGACAATGCCTGGATC 4320
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Db     4706 GGCATGGAGGTGTACAAAGGCTACATGGATGACCCGAGGAACACGGACAATGCCTGGATC 4765
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Qy    4321 GAGACGGTGGCCGTCAGCGTCCACTTCCAGGACCAGAATGACGTGGAGCTGAACAGGCTG 4380
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Db    4766 GAGACGGTGGCCGTCAGCGTCCACTTCCAGGACCAGAATGACGTGGAGCTGAACAGGCTG 4825

Qy    4381 AACTCTAACCTGCACGCCTGCGACTCGGGGGCCTCCATCCGATGGCAGGTGGTGGACAGG 4440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4826 AACTCTAACCTGCACGCCTGCGACTCGGGGGCCTCCATCCGATGGCAGGTGGTGGACAGG 4885

Qy    4441 CGCATCCCACTCTATGCGAACCACAAGACCCTCCTCCAGAAGGCAGCCGCTGAGTTCGGG 4500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4886 CGCATCCCACTCTATGCGAACCACAAGACCCTCCTCCAGAAGGCAGCCGCTGAGTTCGGG 4945

Qy    4501 GCTCACTACTGA 4512
           ||||||||||||
Db    4946 GCTCACTACTGA 4957
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=> s penner reinhold/au
L1          129 PENNER REINHOLD/AU

=> s fleig andrea/au
L2           76 FLEIG ANDREA/AU

=> s ltrpc2 (s) screen?
L3            3 LTRPC2 (S) SCREEN?

=> dup rem 13
PROCESSING COMPLETED FOR L3
L4            3 DUP REM L3 (0 DUPLICATES REMOVED)

=> d 14 total ibib
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L4   ANSWER 1 OF 3   CAPLUS   COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:320077   CAPLUS
DOCUMENT NUMBER: 138:331656
TITLE: Method for screening cell death inhibitor
INVENTOR(S):   Sano, Yorikata; Inamura, Kohei; Miyake, Akira; Yokoi,
                           Hiromichi; Nozawa, Katsura; Mochizuki, Shinobu
PATENT ASSIGNEE(S):   Yamanouchi Pharmaceutical Co., Ltd., Japan
SOURCE: PCT Int. Appl., 98 pp.
                           CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

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    PATENT NO.          KIND  DATE         APPLICATION NO.   DATE
    ---------------     ----  --------     ----------------  --------
    WO 2003033727       A1    20030424     WO 2002-JP8128    20020808
        W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
            CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
            GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS,
            LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL,
            PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA,
            UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
            TJ, TM
        RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
            CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
            PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
            NE, SN, TD, TG
```
PRIORITY APPLN. INFO.:   JP 2001-315339   A   20011012
                                         JP 2002-21175   A   20020130
REFERENCE COUNT: 6   THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS
                                 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4   ANSWER 2 OF 3   CAPLUS   COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:575231   CAPLUS
DOCUMENT NUMBER: 137:119632
TITLE: Screening for modulators of human Ca2+-ATP regulated
                           long transient receptor potential channel (LTRPC7)
INVENTOR(S):   Penner, Reinhold; Fleig, Andrea
PATENT ASSIGNEE(S):   The Queen's Medical Center, USA

```
SOURCE:                     PCT Int. Appl., 80 pp.
                            CODEN: PIXXD2
DOCUMENT TYPE:              Patent
LANGUAGE:                   English
FAMILY ACC. NUM. COUNT:  1
PATENT INFORMATION:

      PATENT NO.        KIND  DATE            APPLICATION NO.  DATE
      --------------    ----  --------        ---------------- --------
      WO 2002059307     A2    20020801        WO 2001-US47784  20011113
      WO 2002059307     A3    20030605
         W:  AU, CA, JP
         RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
            PT, SE, TR
      EP 1337635        A2    20030827        EP 2001-270129   20011113
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, FI, CY, TR
PRIORITY APPLN. INFO.:                        US 2000-248235P  P  20001113
                                              US 2000-254468P  P  20001208
                                              WO 2001-US47784  W  20011113


L4    ANSWER 3 OF 3   CAPLUS   COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:           2002:368512   CAPLUS
DOCUMENT NUMBER:            136:363809
TITLE:                      Protein and cDNA sequences of a novel human long
                            transient receptor potential channel (LTRPC2
                            ) and methods of screening for its
                            modulators
INVENTOR(S):                Penner, Reinhold; Fleig, Andrea
PATENT ASSIGNEE(S):         The Queen's Medical Center, USA
SOURCE:                     PCT Int. Appl., 60 pp.
                            CODEN: PIXXD2
DOCUMENT TYPE:              Patent
LANGUAGE:                   English
FAMILY ACC. NUM. COUNT:  1
PATENT INFORMATION:

      PATENT NO.        KIND  DATE            APPLICATION NO.  DATE
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      WO 2002038608     A2    20020516        WO 2001-US47331  20011113
      WO 2002038608     A3    20030313
      WO 2002038608     C2    20030530
         W:  AU, CA, JP
         RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
            PT, SE, TR
      AU 2002028903     A5    20020521        AU 2002-28903    20011113
      US 2002182635     A1    20021205        US 2001-7706     20011113
      EP 1334129        A2    20030813        EP 2001-990026   20011113
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, FI, CY, TR
PRIORITY APPLN. INFO.:                        US 2000-248442P  P  20001113
                                              US 2000-254528P  P  20001208
                                              WO 2001-US47331  W  20011113
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